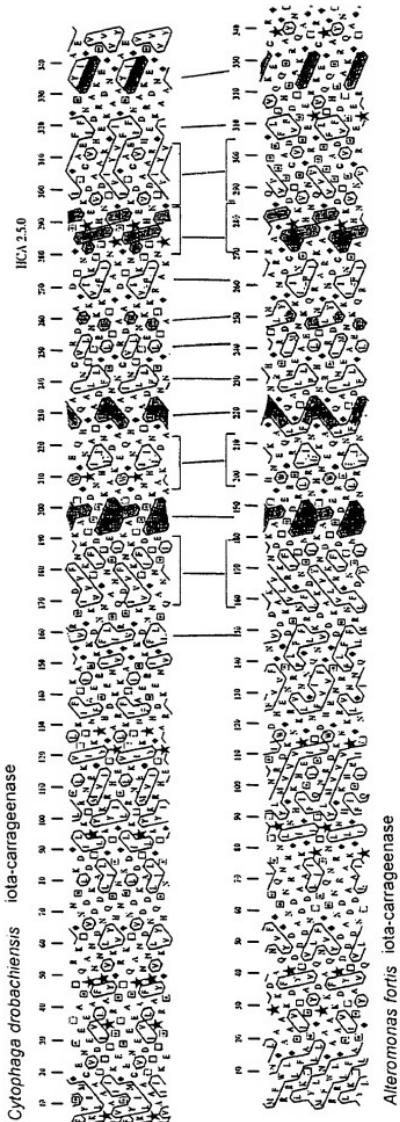


↓ ↓ ↓

27	AVSPKTYKDADFYVAPTOQDVY	DLVDDFGANGNDTSD	64
28	DISEI SEVPTELRAAASSFYTPPGQNV RANKNLVIDYGVNHNDQND		74
65	DSNALQRRAINAI SRKPNGGILLIPNGTYHFLGIQMKS NVH IRVESDVI IK		114
75	DS SKINLAI KDSL DTGGILITPKGKYYLTKIRMR SNVHLEIEKGIV TY		122
115	PTWN GDGKNHRLFEVG VNNIVRNFSFQGLGNGLVDFKDSRDKNLA V		161
123	PTKGLUTPAKNHRI FDPASKTEKEIENASTVKGKGP TVDLRCNSSKNQIV		172
162	FKLG D VRNYKISNFTIIDDKITIFASILV D VTERNRLHWSRNGLIERIK Q		211
173	ADVGNVINFKISNFTIKDEKTIFASILVSPIDKAGN AWP HKGII ENIDQ		221
212	NNALFGYGLI QTGYGADN ILFRNLHSEGGLIA LRMETDNLLMKN YKQGGIR N		261
222	ANAHIGYGLI QAYAADN ILFNNL S CTGGVTLRLETDNLAMKTAKKGGVR D		271
262	I PAFINIRCSKGLAA VMFGPHFMKNGD VQV INVSSVSCGS A VRSDSGFVEL		311
272	I FA I KIKN NINGLTPVMFSPHFMENGKV T IDVTAIC CAYAVR VEHGFIE I		321
312	FSP TDEV HIRQ SWKQ AVESKL GRGC AQT P VARG NG GTRWAAR VT QKD		358
322	F DKG NRASA D AFKN YI EGIL GAGS VEV VYKR NNG RT WAARI AND FNEA		369
359	A CLD KAKLEY GIE PG SFG T KVFDV TARF GYNADL KQD QLDY FSTS NPM		407
370	A YNH S NP AVSG I KPGK FAT SKV INVK ATYKG TGA KLQ AFL SYL PC SER		418
408	C KR VCL PT KEQ NSK QG QI YIGPSL AAVID TTPET SKYD YD V KTF NV KRI		457
419	S K VCR EGP DGF E YNGPSL GVT II NIKR D NSL QN YN NVN VST SSV Q		462
457	NFP VN SHK T ID INT ESS RV CN YY QMSEC SSS RWER		491
463	GFP NN VLV NK YNT PKV CN QNL G SIT SCN		491

FIG.1

FIG. 2



1	MKCKPNFYGKMGRITALSSLFYFLGLVYGOOPTKTSNPNDQWTIKWSASDEFN_KNDPDW	59
1	MKPISIVAFPIPAISMLLSAVSQAASM_QPPIAK_PGETWILQAKRSDEFNVK_DAT	55
60	AKWIK_TGNLPNTSAWKWN_NOKNVKISNGIAELTM_RHNANNTPPDGGT_____YF	108
56	_KWNFQTENYGVWS_WK_NENAT_V__SNGKLKLTTKRESHQRIFWDGCNQQQVANYPLY	109
109	TSGIFKSYQKFYTYGFEAKIQGADIGEVCPSEWLSDFDYSVAN_GETVYSEIDVVEL	166
110	YTSGVAKSRATGNYYGYEARIKGASTFFPGVSPAFWMYSTIDRSLTKEGDVQYSEIDVVEL	169
167	QQFDWY_EGHQDDIYDMDLNLHAVVKENGQGVWKRPKMYPQEQLNKWRAM_DPSKDFHIY	224
170	TQKSAVRES_DH_DLH_NI_VVK_NGKPTWMRPGSFPTNHNGYHLPFDPRNDFHTY	221
225	GCEVNQNIEIHWYDGVE_VARKPNKYWHRPMNVTLSLGLRKPFVKFFDNKNNAINPETDA	283
222	GVNVTOKITWYVDG_EIVGEKDNLWHRQMNLTLSQGLRAPHTQW_KCNQFYP SAN	276
284	K_AREKLSDIPTSMYDVYRVWEKSAGNTTNPPTEVGTLKTKGSKLVIDHWDASTGTIS	342
277	KSA_EGF_PTSMEVYDVRIWVKVGNNSAPGEGQSCPNTFVAVNSVQLSAAKQTLRKG	332
343	AUSNNIKTGQYAGSVNNASIAQIVTLKANTSYKVSAGKASSEGTSAYLGISKASNNELI	402
333	QSTITLESTVLPNCATNNKKVISSSNKNVATVNSAGVV_KAKNKGTTATITVKTGNKGKIDKL	392
403	SNFEFKTTSYSKGEIEIRTGNVQESYRIVWSSGQAYCDDFNLVIEINSASQLNESETET	462
393	TIAVN	397
463	ALEKGIIHYPNPYKNGPLTIDFGKPFSGEVQITGLNGRTFLRRNNVDQTSVQLLESKSKF	522
523	KSGLYIIVKISGPGEVSKKILVE	545

FIG.3

FIG. 4

